

Privacy Audits for Clinical Large Language Models

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Abstract

Large language models (LLMs) fine-tuned on de-identified clinical notes raise privacy concerns because automated de-identification can leave residual patient identifiers in the training data. We study whether such identifiers can be recovered from a fine-tuned model using query access alone as a function of query budget. We introduce Verified Extraction, an auditing framework that distinguishes identifiers attributable to fine-tuning data from spurious or prior-driven outputs and quantifies recoverable leakage under explicit query budgets. Using MIMIC-IV-Note as the fine-tuning dataset, we find that verified leakage is negligible at small query budgets but becomes practically significant under repeated querying, even when only a small fraction of identifiers remains in the training data. These results highlight the importance of privacy evaluations that account for repeated-query access rather than one-off prompt tests.

1. Introduction

Large Language Models (LLMs) trained or fine-tuned on clinical data support clinical decision-making, diagnostics, and medical workflows, typically by adapting general-purpose foundation models to medical corpora such as Electronic Health Records (EHRs). Clinical notes—a key EHR component—contain rich, heterogeneous information about patients’

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medical histories, social and family contexts, and care trajectories (Demner-Fushman and Elhadad, 2016). They document patient history, symptoms, examination findings, diagnostic results, and treatment plans. With the advent of LLMs, clinical notes are increasingly leveraged across clinician-facing, administrative, and research applications, including summarizing longitudinal records (Adams et al., 2021), generating patient-facing texts tailored to different health literacy levels (Sinha et al., 2023), and extracting structured information and performing downstream analytics (Ben Shoham and Rappoport, 2023; McInerney et al., 2024; Agrawal et al., 2022; Goel et al., 2023). While some clinical LLMs are released as open source (Chen et al., 2023; Sellergren et al., 2025), many remain accessible only via APIs (Jiang et al., 2023; Peng et al., 2023; Saab et al., 2024), often due to privacy concerns or the protection of institutional knowledge.

With clinical notes as a primary source of training for LLMs, new privacy challenges arise even when the models are only available via API and query access. The privacy concerns stem from language models’ ability to memorize and reproduce training data (Carlini et al., 2021, 2019); fine-tuning can further amplify this effect by increasing the output likelihood for rare, patient-specific information (Lukas et al., 2023; Chen et al., 2024b). To mitigate this risk, any personal identifiers, such as patient names, are removed from clinical notes—the process called *de-identification*—before they are used in training. The de-identification process is typically automated.

In practice, de-identification of clinical notes is often imperfect. State-of-the-art automated tools achieve only up to 99% F1 (Tannier et al., 2024; Chen et al., 2024a), thus residual identifiers can remain at scale. Prior work has investigated whether such residual personal information can leak from clinical language models, with mixed conclusions depending on task and threat model (Lehman et al., 2021; Huang et al., 2022; Lukas et al., 2023). A key gap is that much of this evidence is conservative (e.g., showing limited extraction under simple probes) or based on coarse comparisons of scrubbing interventions. As a result, it does not reflect the real risk to patient privacy.

We re-examine the risk that clinical LLMs leak explicit personal identifiers (e.g., patient names) from an operational auditing perspective. Because real-world attackers face cost and access constraints, they cannot issue unlimited queries; we therefore model attacks using a query budget, defined as the maximum number of queries allowed. Specifically, we ask: *Given an LLM fine-tuned on clinical notes with a known level of residual identifiers, can an auditor or attacker—restricted to query-only access and a limited query budget—reliably recover those identifiers?* We define the *residual direct identifier rate* as the ratio of direct identifier mentions remaining after de-identification to the total number of such mentions in the original clinical notes.

To answer this question, we split the problem into three steps: risk measurement, extraction, and verification. We separate these steps because the discovery of an identifier in the model’s output is not always sufficient to claim a privacy leak: the model can also generate realistic-looking identifiers that were never in the fine-tuning data. We proceed in three stages. **First**, we evaluate whether fine-tuning increases the baseline likelihood that direct identifiers (DI) present in the fine-tuning data are emitted in model outputs when prompted, across varying residual direct identifier rate. This establishes whether fine-tuning meaningfully elevates the *risk of direct identifier leakage* in the first place. **Second**, we evaluate *extraction* by prompting the model to generate candidate identifiers, capturing

the attacker’s ability to elicit identifier-like strings through repeated querying. **Third**, we perform *verification*, determining whether each extracted candidate actually originates from the fine-tuning data rather than being a plausible but non-member identifier. This step uses techniques from membership inference attacks (MIAs) to control false positives.

We combine extraction and verification into a single pipeline, which we call **Verified Extraction**, and derive formulas that predict how many verified identifiers an attacker can recover given a query budget.

We experimentally evaluate our audit approach on the MIMIC-IV-Note dataset in a realistic large-scale setting, using models with one billion (1B) and eight billion (8B) parameters, fine-tuned on $\sim 300k$ notes with varying levels of residual patient names. We focus on patient names as they appear in every clinical note, often at multiple places, and hence some are likely to be missed by automated de-identification tools at scale. For the 1B model, when the residual direct identifier rate (of patient names) is about 10%, we find that an attacker can recover 3% of those names with 95% precision by using on the order of 10^7 model queries—corresponding to roughly \$1K at contemporary consumer-model API pricing.¹ We then find that the larger 8B model exhibits even higher verified leakage; across residual direct identifier rates from 1% to 10%, the observed increase ranges from $7.8\times$ to $152.0\times$ with 10^5 queries. These results demonstrate that even small de-identification errors can lead to practically significant patient identifier leakage under repeated querying, and that this risk is amplified by model scale.

We make the following contributions:

- **A high-precision privacy audit for clinical LLMs.** We introduce *Verified Extraction*, an auditing framework for direct identifier leakage that combines repeated-query extraction with membership-based verification, allowing candidate identifiers surfaced by a model to be filtered for likely attribution to the fine-tuning data.
- **Analytical leakage estimation under repeated querying.** We derive formulas for estimating how leakage—defined as the number of direct identifiers that can be both extracted and attributed to the fine-tuning data—scales with attacker query budget, and show that this analysis closely matches empirical sampling results.
- **Empirical evidence that leakage grows with residual identifier rate, query budget, and model scale.** In large-scale clinical fine-tuning experiments on the MIMIC-IV-Note dataset of 300k notes, we show that verifiable identifier extraction becomes practically significant as residual direct identifier rate increases, quantify attacker effort in both query count and dollar cost, and find that an 8B model exhibits substantially higher leakage than a 1B model at the same budgets.

Generalizable Insights about Machine Learning in the Context of Healthcare

- **Privacy risk in healthcare foundation models is shaped by attacker budget and access constraints, not only by whether a model can leak in a single probe.** Evaluations based only on limited prompting can underestimate real-world risk when repeated querying is feasible.

1. Cost estimates are provided for interpretability and depend on the model and provider; we assume a cost of \$5 per million tokens, based on the price of OpenAI GPT-4.1 mini as of February 1, 2026.

- **Small upstream de-identification errors can remain consequential after model training.** In healthcare ML pipelines, imperfect preprocessing of sensitive clinical text should be treated as a quantitative source of downstream privacy risk rather than as a binary pass/fail safeguard.
- **Auditing generative models in healthcare requires verification in addition to generation.** Because models can produce plausible but non-member identifiers, reliable privacy evaluation should combine candidate extraction with methods that assess whether outputs are attributable to the training data.

Data and Code Availability

This paper uses the MIMIC-IV-Note dataset (Johnson et al., 2023), which is available on the PhysioNet repository (Goldberger et al., 2000).

Code is available at: <https://github.com/G2Lab/verified-extraction-audit>. The online README includes a step-by-step guide to reproduce our results, with MIMIC access. The code can also be adapted to a new dataset and to any LLM model for new audits (see the README). Fine-tuning details are in Appendix A.

2. Related work

Memorization, extraction, and budget-aware risk. A substantial literature demonstrates that language models can memorize and reproduce parts of their training data. Carlini et al. introduced *canary insertion* and *exposure* to quantify memorization via the probability mass assigned to rare, uniquely identifiable sequences (Carlini et al., 2019), and later showed that memorized training examples could be *extracted* at scale using prompting and stochastic sampling (Carlini et al., 2021). More recently, Hayes et al. argued that one-shot extractability was an incomplete view for stochastic generators and proposed *probabilistic discoverable extraction*, which measured how recovery probability grows with the number of generations (i.e., attacker query budget) (Hayes et al., 2025). Building on this budget-aware perspective, we focus on direct identifiers in clinical fine-tuning and frame extraction as an audit: repeated querying is used to generate candidate identifiers, which are then verified to control false positives.

Direct identifier leakage in language models and training data de-identification of clinical data. Prior work has studied direct identifier leakage from language models using game-based notions such as extraction, inference, and reconstruction. Lukas et al. empirically showed that curating training data by removing direct identifiers reduced—but did not eliminate—leakage across multiple domains, including healthcare (Lukas et al., 2023). Lehman et al. examined Protected Health Information (PHI) leakage from a BERT model pretrained on MIMIC-III notes and found that simple probing did not meaningfully extract PHI, while noting that more sophisticated attacks might be plausible (Lehman et al., 2021). Related work further distinguished between *memorization* and *association* in personal-information leakage: Huang et al. showed that models might memorize personal strings while being less effective at linking them to specific individuals from context (Huang et al., 2022). Complementary research in clinical Natural Language Processing (NLP) evaluated de-identification systems directly by measuring residual identifiers and redaction

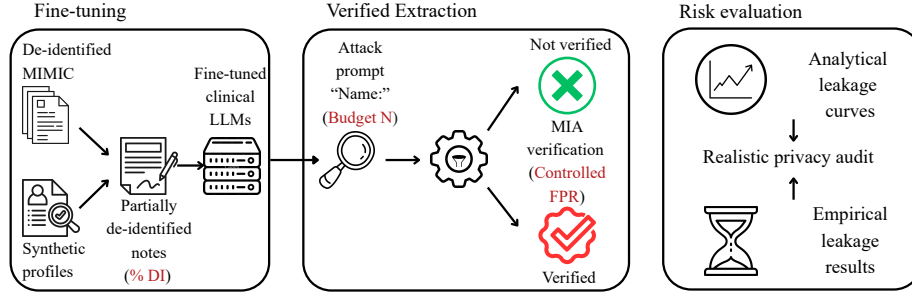


Figure 1: Overview of our Verified Extraction Pipeline.

performance in the clinical text that could be used by LLMs for fine-tuning (Larson et al., 2024). Our work connects these lines of research by treating imperfect de-identification as a realistic starting point and measuring how repeated querying of a fine-tuned model changes which direct identifiers become extractable.

Membership-Inference Attacks (MIAs) as verification for privacy auditing. MIAs ask whether a specific record was included in a model’s training set, providing an auditing primitive with explicit operating characteristics such as True Positive Rate (TPR) at controlled False Positive Rate (FPR) (Shokri et al., 2017). For text generation, Song et al. developed MIAs to audit data provenance in generative models, illustrating how membership signals could support attribution beyond surface string matching (Song and Shmatikov, 2019). Recent work revisited MIAs for modern LLMs and proposed stronger auditing methodologies and pipelines under different access assumptions (Duan et al., 2024; Wen et al., 2024; Panda et al., 2025; Rossi et al., 2025).

Membership inference without shadow models MIAs test whether a candidate clinical note was used during training, providing a privacy signal complementary to verbatim extraction. In language-model settings, a common family of MIAs is *loss-based*, exploiting the fact that training examples tend to have lower negative log-likelihood under the fine-tuned model than non-members. A simple loss-threshold attack predicts membership when $\ell_{\text{ft}}(x) \leq \tau$ where $\ell_{\text{ft}}(x)$ denotes the negative log-likelihood of candidate x under the fine-tuned model (Yeom et al., 2018). In gray-box audits, membership evidence can be strengthened by comparing the fine-tuned model to a reference (e.g., the base model) via a likelihood-ratio style score, $s(x) = \ell_{\text{base}}(x) - \ell_{\text{ft}}(x)$, where larger $s(x)$ indicates that fine-tuning makes x substantially more likely.

This contrasts with the classical MIA framework, which trains an attack classifier by using *shadow models* to approximate the target model’s behavior (Shokri et al., 2017). Loss-based MIAs align naturally with auditing under gray-box access because they operate directly on model scores and do not require training multiple auxiliary models.

Our paper combines budgeted extraction with score-based membership verification to estimate budget-conditioned leakage curves that represent the number of direct identifiers that can be extracted and verified under a given attacker query budget.

3. Methods

3.1. Problem setup

We study the leakage of personal information from large language models fine-tuned on partially de-identified clinical notes. Clinical notes may contain multiple classes of sensitive attributes, including *direct identifiers* and *quasi identifiers*. Direct identifiers uniquely identify an individual on their own (e.g., full names), whereas quasi identifiers may not be unique in isolation but can enable re-identification when combined with auxiliary information (e.g., age, ZIP code, rare diagnoses). We focus on *direct identifier leakage*, specifically patient names that appear in the metadata and often the text of clinical notes. Our goal is to operationalize private information leakage risk in a way that matches adversarial behavior: rather than asking whether *any* identifier can be elicited under ad hoc prompting, we measure how frequently identifiers are revealed when an attacker repeatedly queries the model using a fixed decoding strategy.

Privacy risk depends strongly on the interface available to an auditor or attacker. In a *black-box* setting, one observes only prompts and generated text. In a *gray-box* setting, one additionally observes token-level log probabilities for a set of alternative text completions of the same prompt, enabling likelihood-based scoring without access to model weights. In a *white-box* setting, one has access to model parameters. Our methods target gray-box auditing, which is a realistic setting for LLMs available via provider APIs.

We summarize attacker capability by a *query budget* N . The attacker (or auditor) issues N queries using a fixed prompt template and fixed decoding strategy (e.g., repeatedly sampling completions of a prompt such as `Name:`), yielding N generations. Under repeated sampling, even identifiers with a low probability of being generated in the LLM outputs may eventually appear; consequently, leakage is determined by (i) the residual direct identifier rate in the fine-tuning data and (ii) the attacker’s query budget; increasing either can increase the expected number of extracted direct identifiers.

The overview of our pipeline is presented in [Figure 1](#).

3.2. Dataset

We use the MIMIC-IV-Note dataset ([Johnson et al., 2023](#)), made up of 331,794 de-identified discharge summaries from 145,915 patients. We split the notes into training, validation, and test sets, ensuring no patient overlap between the sets, as shown in [Table 1](#).

3.3. Controlled Direct Identifier Injection

To evaluate the risk of direct identifier leakage in language models trained on clinical notes, we developed a controlled direct identifier injection pipeline that systematically replaces masked direct identifiers in MIMIC-IV discharge summaries with synthetically generated direct identifiers. For each patient in the dataset, we generate a corresponding persona containing synthetic direct identifier attributes that match the patient’s demographic characteristics. Our persona generation system uses the Faker library ([Faraglia, 2026](#)) to sample locale-specific names from the census data of multiple countries.

A fundamental challenge in automated direct identifier injection is to determine which type of direct identifier should be inserted at each masked location. Clinical notes contain

Table 1: Dataset splits for MIMIC-IV-Note.

Split	# Notes	# Patients
Train	268,303	118,190
Val	29,537	13,133
Test	33,954	14,592

Table 2: Distinct names per direct identifier (DI) rate and split.

DI rate	Split	# Distinct names
1%	Train	9,710
5%	Train	40,467
10%	Train	68,730
100%	Train	234,904
All	Val	25,990

diverse direct identifier types (i.e., patient names, physician names, dates, age, etc), each requiring different synthetic values from distinct persona attributes. We use Gemini 2.5 Flash to classify each masked direct identifier slot into semantic categories. This produces tag files that map each direct identifier slot identifier to its semantic category.

After classification, we perform controlled direct identifier injection using probabilistic sampling. For each note, we iterate through all classified identifier slots and independently sample each slot with probability p_{DI} . This stochastic sampling ensures that only a subset of direct identifier slots are replaced in each note, creating realistic scenarios where some direct identifiers are present while other slots remain masked. We created four datasets with $p_{DI} \in \{1\%, 5\%, 10\%, 100\%\}$, as shown in Table 2.

To assess whether the injected name strategy mimics realistic de-identification systems, we re-ran two de-identification tools on the notes after synthetic name insertion: Presidio (Mendels et al., 2018), a general-purpose de-identification system, and pyDeid (Sundrelingam et al., 2024), a clinical-domain de-identification system. Presidio left approximately 4% residual direct identifiers, while pyDeid left approximately 8%. Both tools also exhibited partial per-instance de-identification, where the same name was redacted in some locations but missed in others. This suggests that the injected names preserve enough contextual and grammatical realism to induce imperfect, non-uniform redaction patterns consistent with the threat model we study.

3.4. Fine-tuning details

We fine-tuned the Meta Llama 3.2 1B and Meta Llama 3.1 8B general-purpose models (Llama Team, AI Meta, 2024) on the MIMIC-IV clinical notes with injected synthetic direct identifiers using supervised fine-tuning (SFT). Our implementation follows the Stanford Alpaca framework (Taori et al., 2023). Each training example consists of an instruction field (“Generate a clinical note”) and an output field containing the complete clinical note text. The data is formatted using Alpaca-style prompt templates that structure the input as “### Instruction:”, followed by the instruction text, and “### Response:”, followed by the model’s expected output. While the explicit task is to generate clinical notes from instructions, this fine-tuning process also serves as domain adaptation, enabling the model to learn clinical terminology, note structure, and domain-specific patterns from the MIMIC-IV corpus. To prevent overfitting, we monitor model perplexity on held-out validation data throughout training. Models are fine-tuned using full parameter fine-tuning.

3.5. Privacy risk quantification

3.5.1. AUDIT SETTING AND THREAT MODEL

Our goal is to design a realistic *audit* that approximates private information leakage under a plausible attack scenario: rather than asking whether any identifier can be elicited under ad hoc prompting, we quantify how direct identifier leakage scales with attacker’s capability, defined as a query budget N . Given a fixed prompt, an LLM defines a distribution over candidate continuations. Decoding settings determine how this distribution is transformed into a realized completion, thereby affecting which continuations are observable and their associated probabilities.

We assume *gray-box* access to the fine-tuned LLM at inference time: the auditor can issue prompts and obtain both generated text and token-level log probabilities for candidate continuations under fixed decoding settings. These token-level log probabilities for candidate continuations are available with some LLM providers like OpenAI. The auditor does not access model weights.

To control false positives, *i.e.*, the direct identifiers that are in the outputs but not from the fine-tuning data, our audit uses a classifier (that we call *verifier*) predicting membership of the generated direct identifiers using MIA techniques. We assume the auditor has access to a labeled subset of identifiers from the fine-tuning split (*train*) and from a disjoint held-out split (*val*) to train this classifier. The labels indicate whether the identifiers are present or not in the fine-tuning dataset. The auditor can build such a labeled set by manually checking some notes and annotating the missed identifiers. These labels are used only for verification; extraction itself is performed by querying the model. We evaluate the verifier via cross-fitting (Chernozhukov et al., 2024) ensuring that each candidate direct identifier is scored by a verifier that did not train on that direct identifier.

The auditor issues N independent queries drawn from a fixed prompt distribution (e.g., repeated completions of a templated **Name:** prompt), yielding an *extracted stream* of candidate identifiers whose composition evolves with N . An identifier is considered leaked only if it is surfaced by extraction and accepted by the verifier.

Note that our internal audit framework also corresponds to an external attacker threat model with insider knowledge, who has access to a small labeled dataset. This is a strong but common threat model in MIA literature (Shokri et al., 2017).

We next formalize how extraction and verification combine to yield *budget-conditioned* leakage curves that can be predicted from model scores, avoiding prohibitively large numbers of sampled generations.

3.5.2. ANALYTICAL CHARACTERIZATION OF BUDGET-CONDITIONED LEAKAGE

Setup and notation. Let $\mathcal{U}$ denote a universe of candidate identifiers (patient names) considered by the audit. Each candidate $i \in \mathcal{U}$ has a membership label $y_i \in \{0, 1\}$, with $\mathcal{T} = \{i \in \mathcal{U} : y_i = 1\}$ (train members) and $\mathcal{V} = \{i \in \mathcal{U} : y_i = 0\}$ (held-out non-members).

We consider an extraction procedure that issues N *independent* queries drawn from a fixed prompt distribution and decoding settings, producing a *stream* of candidates. We assume independence because each LLM query does not reuse the context from previous queries, as highlighted in (Hayes et al., 2025).

Per-candidate extraction probabilities from model scores. For each candidate identifier i , let $p_i \in (0, 1]$ denote the per-query probability that the model emits i under the fixed extraction protocol. Each p_i is non-zero because of the absence of filtering. In our gray-box setting, p_i can be estimated from model log probabilities for candidate continuations (e.g., by scoring the candidate string under teacher forcing as described in the next section) (Yi and Li, 2026; Janicki et al., 2026). These p_i values serve as deterministic inputs to the leakage curves below, enabling prediction without requiring prohibitively many sampled generations.

Budgeted unique-hit probability. Let $E_i(N)$ be the event that identifier i appears at least once in N independent generations. “The candidate is emitted at least once” can be modeled as evaluating the Cumulative Distribution Function (CDF) at N of a geometric distribution because each query is independent: $\Pr(E_i(N)) = 1 - (1 - p_i)^N \triangleq \pi_i(N)$. Intuitively, $\pi_i(N)$ increases with N and transitions from $\pi_i(N) \approx Np_i$ when $Np_i \ll 1$ to $\pi_i(N) \approx 1$ when $Np_i \gg 1$.

Verification model. Each extracted candidate is assigned a verifier score $s_i \in \mathbb{R}$ (e.g., from a membership inference classifier). For a threshold τ , the acceptance rule is $q_i(\tau) = \mathbf{1}\{s_i \geq \tau\}$. A candidate is counted as a *verified leak* if it is extracted at least once (event $E_i(N)$) and accepted by the verifier ($q_i(\tau) = 1$).

Expected verified leakage counts. The expected number of verified true positives (members) and false positives (non-members) are

$$\text{TP}(N, \tau) = \mathbb{E} \left[\sum_{i \in \mathcal{T}} \mathbf{1}\{E_i(N)\} q_i(\tau) \right] = \sum_{i \in \mathcal{T}} \pi_i(N) q_i(\tau) \quad (1)$$

$$\text{FP}(N, \tau) = \mathbb{E} \left[\sum_{i \in \mathcal{V}} \mathbf{1}\{E_i(N)\} q_i(\tau) \right] = \sum_{i \in \mathcal{V}} \pi_i(N) q_i(\tau) \quad (2)$$

The expected number of accepted candidates is $A(N, \tau) = \text{TP}(N, \tau) + \text{FP}(N, \tau)$.

Budget-conditioned rates on the extracted stream. To report verifier performance in the attacker-relevant regime (conditioned on candidates that are actually surfaced), we use extracted-stream rates, with $E(N) \triangleq \{E_i(N)\}_{i \in \mathcal{U}}$ the vector of extraction indicators across all candidates:

$$\text{TPR}_{\text{ext}}(N, \tau) = \Pr(\hat{y} = 1 \mid y = 1, E(N) = 1) \quad (3)$$

$$= \frac{\text{TP}(N, \tau)}{\sum_{i \in \mathcal{T}} \pi_i(N)}, \quad (4)$$

$$\text{FPR}_{\text{ext}}(N, \tau) = \Pr(\hat{y} = 1 \mid y = 0, E(N) = 1) \quad (5)$$

$$= \frac{\text{FP}(N, \tau)}{\sum_{i \in \mathcal{V}} \pi_i(N)}, \quad (6)$$

with the convention that the ratio is undefined if the denominator is zero. Unlike standard candidate-uniform MIA reporting, these rates are *stream-weighted* by $\pi_i(N)$ and therefore vary with the attacker budget N .

Critical budget. The scale Np_i governs the budget. A candidate becomes likely to appear once N exceeds its *critical budget* $N_i^* \approx 1/p_i$ (up to constant factors). As N increases, candidates enter the extracted stream in decreasing order of p_i , so leakage can exhibit a sharp rise when N crosses the range of N_i^* for a large mass of identifiers.

3.5.3. EXTRACTION

Per-name emission probabilities from teacher forcing. To instantiate the analytical framework, we estimate the per-query emission probability of each candidate name $i \in \mathcal{U}$ under a fixed extraction prompt. Concretely, we score each candidate continuation under **Name:** using teacher forcing, yielding a model-implied probability p_i^{ft} for the fine-tuned model. We compute the analogous probability p_i^{base} for the corresponding base (pre-fine-tuning) model under the *same* prompt and tokenization.

Relative amplification through fine-tuning. To summarize how fine-tuning changes the emission of identifiers, we compute a per-name emission multiplier $r_i \triangleq \frac{p_i^{\text{ft}}}{p_i^{\text{base}}}$. We report robust summaries (e.g., tail percentiles) of $\{r_i\}$ over train and held-out name sets.

Sampling-based extraction experiments. To validate our analytical characterization with direct sampling, we run a generation-based attack using the same prompt template. For each query, we sample a completion of length 20 tokens with temperature 1.0 and without top- k or top- p filtering. We repeat this procedure N times (query budget), and parse each completion by taking the first two words as a candidate name. This heuristic for parsing may miss some real-world failure modes, but it still allows us to reliably estimate a meaningful lower bound on the potential leakage.

3.5.4. VERIFICATION - MIAS

Verifier model and features. To verify whether an extracted candidate identifier is likely to originate from the fine-tuning cohort, we train an MIA verifier that maps each candidate name i to a score s_i . Our verifier is a logistic regression trained on four gray-box features derived from model probabilities under teacher forcing: (i) p_i^{ft} under the **Name:** prompt, (ii) p_i^{base} under the **Name:** prompt, (iii) p_i^{ft} under the **Patient:** prompt, and (iv) p_i^{base} under the **Patient:** prompt. We include the additional **Patient:** prompt because it empirically slightly improves verifier separability, likely by providing a second, clinically natural context in which memorized identifiers exhibit membership-specific likelihood shifts. In any case, this simple four-feature verifier makes our extraction numbers a lower bound, since a motivated attacker could potentially develop stronger methods.

Cross-fitting to avoid contamination. To prevent optimistic bias from scoring candidates that were seen during verifier training, we use K -fold cross-fitting with $K = 5$. We partition the labeled candidate set into folds; for each fold, we train the verifier on the remaining folds and compute out-of-fold scores for the held-out fold. This yields a score s_i for every candidate name that is produced by a verifier that did not train on that name.

Threshold selection and operating point. In each experiment, we choose a decision threshold τ to control false positives. Specifically, for a target budget N we select τ such that the extracted stream false positive rate $\text{FPR}_{\text{ext}}(N, \tau)$ (Equation 6) is below a chosen

level (5% in our experiments). This calibration is important: without an explicit operating point, verification can become overly permissive as the extracted stream shifts with budget.

4. Results

4.1. Fine-tuning increases the risk of name emission

In [Figure 2](#), we quantify how fine-tuning changes the model’s tendency to emit specific identifiers by computing, for each candidate name i , a *relative emission-probability change* under the fixed extraction prompt/decoding described in [section 3](#). For each residual direct identifier rate we summarize the per-name ratios over the corresponding candidate set – names seen during fine-tuning (*train*) or a disjoint held-out set (*val*) – with two complementary statistics, shown as the two panels.

The median (left panel) tracks the typical per-name change. Train and val curves rise together with the residual direct identifier rate and have essentially the same shape, reflecting generalization of a “name prior” rather than name-specific memorization. At low residual direct identifier rates both curves sit well below one: when most names in the fine-tune corpus are replaced by the placeholder `---`, the fine-tuned model learns that the high-probability continuation at name positions is the placeholder, so the per-name emission probability *decreases* on both members and non-members. As the residual direct identifier rate grows and real names become common during fine-tuning, the model re-learns a general name prior and the typical multiplier climbs for both splits.

The 99th percentile (right panel) isolates the extreme tail of the per-name changes, which is the operationally relevant quantity for budgeted extraction: an attacker only needs a small number of names to become orders of magnitude more likely in order to recover them. The same overall trend with the direct identifier rate is visible, but the whole tail is lifted by many orders of magnitude compared to the median.

The memorization signal appears mainly in the extreme tail: while train and val names show similar median trends as the residual direct identifier rate increases, the train–val gap is much larger at the 99th percentile. This indicates that extractable risk is concentrated in a small subset of training names whose emission probabilities are amplified far more than comparable held-out names.

4.2. LLMs fine-tuned on clinical notes are vulnerable to MIAs

Fine-tuning not only increases the probability of emitting name-like identifiers ([Figure 2](#)), but also induces a measurable membership signal that can be exploited to *verify* whether an extracted candidate is likely to originate from the fine-tuning set.

[Figure 3](#) reports Receiver Operating Characteristic curves (TPR vs. FPR) for our MIA verifier at two query budgets, $N = 10^4$ and $N = 10^7$. Importantly, these curves are *budget-conditioned*: rather than evaluating the verifier on a uniformly sampled list of candidate names, we evaluate it on the *extracted stream* induced by running the extraction process for N queries, as defined in [section 3](#). As N increases, the extracted stream includes progressively lower probability and more ambiguous candidates, which changes the operating characteristics of membership inference and typically reduces Area Under the Curve (AUC).

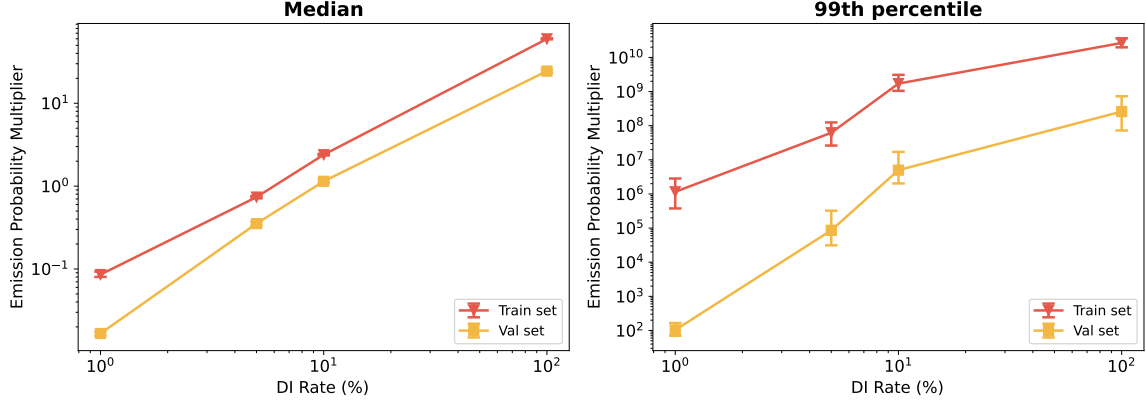


Figure 2: Per-name emission-probability multiplier $p^{\text{ft}}/p^{\text{base}}$ under fine-tuning, summarized by the median (left) and the 99th percentile (right) across candidate names, as a function of the residual direct identifier rate. Red: names seen during fine-tuning (train); yellow: disjoint held-out names (val). Error bars are 95% bootstrap CIs over names. Both curves share the same shape, reflecting generalization of a name prior (and the --- placeholder effect at low rates); the memorization signal is the vertical train/val gap at each direct identifier rate, which is modest on the median but orders of magnitude wider on the 99th percentile, where the true leakage concentrates.

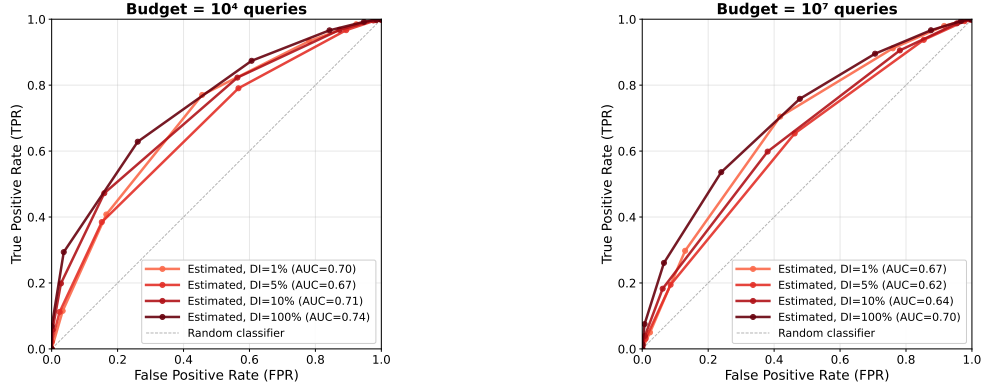


Figure 3: Budget-conditioned MIAs on the extracted names. ROC curves (TPR vs FPR) for the membership-inference verifier are evaluated on candidates surfaced by the extraction process at two query budgets ($N = 10^4$ and $N = 10^7$) and varying residual direct identifier rates, using the analytical framework (“Estimated”).

Overall, the curves show that membership inference provides a substantial advantage over random guessing on the candidates that an attacker would realistically observe at each budget.

Moreover, verifier ablations showed that the main conclusions are robust to several implementation choices. Comparing logistic regression with simple thresholding and varying verifier training set size, we found that differences were small once the verifier was calibrated to the target operating point. The main challenge was not maximizing global discrimination

per se, but calibrating the discrimination signal so that false positives remained controlled on the extracted stream. In practice, all methods stabilized with roughly 1% of labeled candidates, whereas below this level false-positive-rate calibration degraded noticeably. Detailed ablation results are provided in Appendix C.1.

4.3. Direct identifier leakage becomes practically significant beyond a critical budget

Subfigure 4a reports budget-conditioned leakage under Verified Extraction. Across residual direct identifier rates in the fine-tuning data, verified leakage remains negligible at small budgets but increases sharply once the attacker budget crosses a regime where low probability identifiers become likely to appear at least once in the extracted stream.

Higher residual direct identifier rate shifts this onset to smaller budgets and increases the fraction of the direct identifiers in the fine-tuning set that can be recovered. Depending on the residual direct identifier rate, we can recover between 1 and 10% of the names contained in the fine-tuning set. Table 3 summarizes these approximate critical budgets for the 1B model.

The verifier turns raw extraction into an actionable *audit* signal aligned with attacker goals. An attacker (and an auditor) cares not just about seeing name-like strings, but about extracting identifiers that can be credibly linked to the fine-tuning cohort.

Without verification, increases in generated name-like strings could reflect generic name priors or formatting artifacts; with verification, recovered identifiers are accompanied by a membership signal, and subfigure 4b shows that this signal is not triggered at comparable rates on held-out names.

Therefore, Figure 4 shows why privacy risk is *budget-driven*: at small budgets the attack surfaces almost no verified training identifiers, but beyond a critical budget the number of verified leaks rises rapidly (subfigure 4a), while false acceptances remain low (subfigure 4b).

Prompt robustness. Our primary extraction protocol uses direct prompt "Name:" as a stress test. Failure to recover identifiers under such an explicit identifier-elicitation prompt would provide stronger evidence of low risk than failure under a weaker or more natural prompt alone. Importantly, our conclusion is not specific to this prompt. At a large query budget, the softer prompt "Patient:" recovered nearly the same number of verified identifiers across all residual DI rates, and optimally splitting the budget between the two prompts provided only negligible additional gain (the two single prompt estimates differ by at most 4% at $N = 10^{10}$). Thus, within the simple prompt family studied here, the leakage reported for "Name:" is not driven by a single unusually effective prompt (Appendix C.2).

4.4. Scaling

Table 4 shows that the privacy risk identified by Verified Extraction increases substantially with model scale. Across all residual direct identifier rates and both attacker budgets, the 8B model recovers more verified training names than the 1B model. The relative increase is especially pronounced in the low-residual regime: at 1% direct identifier rate, the 8B model recovers 2.24% versus 0.01% at $N = 10^5$ and 6.83% versus 0.06% at $N = 10^6$, corresponding to $152.0\times$ and $116.0\times$ more verified leakage, respectively. Even at more moderate residual

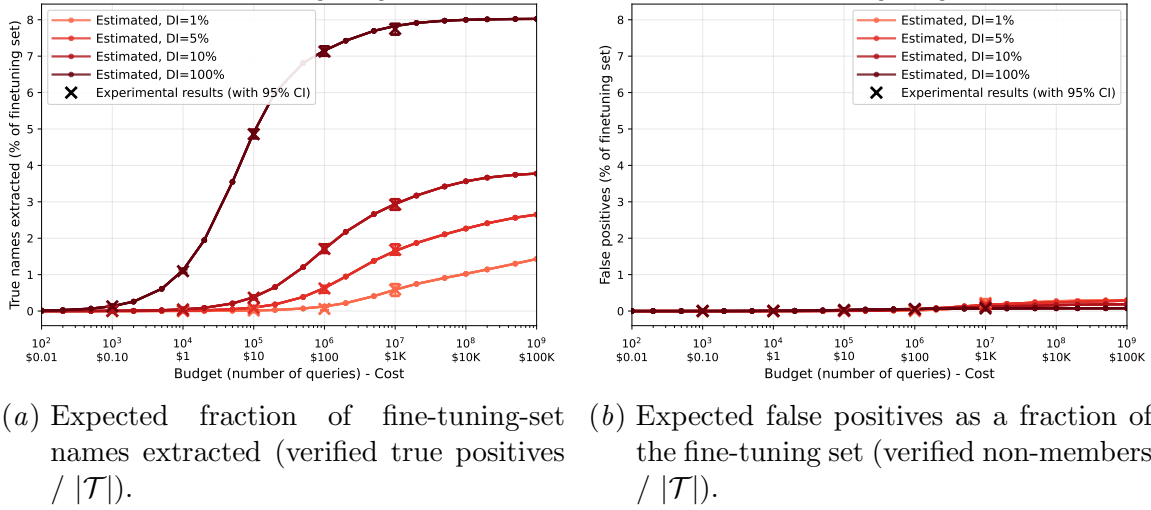


Figure 4: Verified Extraction results as a function of attacker query budget N for different residual direct identifier rates with the 1B model. Curves are analytical predictions computed from the model-implied per-candidate extraction probabilities and verifier scores (section 3); markers show empirical extraction with 95% confidence intervals. A secondary x-axis reports approximate inference cost under our pricing model of \$5 per million tokens (we consider 20 tokens/query; therefore, 10^7 queries = 2×10^8 tokens = \$1,000 at \$5/1M tokens).

rates, the scaling effect remains large; for example, at 10% direct identifier rate and $N = 10^6$, the 8B model recovers 9.80% of training names compared with 1.71% for the 1B model.

The multiplicative gap narrows as the residual direct identifier rate increases, reaching roughly 3–4 $\times$ at 100% direct identifier rate. This suggests that increasing model scale most strongly amplifies leakage in the sparse-identifier regime, where many names remain individually low probability but become substantially more recoverable under a larger model. Operationally, these results imply that privacy evaluations based on smaller models may materially understate risk for larger deployment-scale models, even when the training data and extraction protocol are otherwise unchanged.

5. Discussion

Our methods and results support two key findings. First, we introduce *Verified Extraction*, which extracts direct identifiers from a fine-tuned model and verifies that they match identifiers present in the fine-tuning data. Second, we demonstrate that this approach detects leakage under realistic imperfect de-identification, recovering multiple verified names across a range of residual direct identifier rates and two model sizes.

Our study focuses on the MIMIC-IV-Note dataset (Johnson et al., 2023), but the mechanism of residual direct identifier memorization that we point out is not specific to this dataset. It is a consequence of the next-token prediction loss used in a supervised fine-tuning setting, which increases the probability of emitting these identifiers (Furukawa and Oprea, 2026). Moreover, for our attack queries, we use generic prompts (Name:, Patient:)

Table 3: Approximate critical query budget for the 1B model. Q_{crit} denotes the approximate query budget at which 1% of fine-tuning-set names are verifiably extractable. Values are rounded to the nearest order of magnitude. DI = direct identifier.

DI rate	Q_{crit}
100%	10^4
10%	10^6
5%	10^6
1%	10^8

Table 4: Verified true names extracted as a percentage of the fine-tuning set at two attacker query budgets Q . Ratio = 8B / 1B, computed from unrounded values.

DI rate	Q	1B (%)	8B (%)	Ratio
1%	10^5	0.01	2.24	$152.0\times$
1%	10^6	0.06	6.83	$116.0\times$
5%	10^5	0.08	1.30	$16.0\times$
5%	10^6	0.62	5.51	$8.9\times$
10%	10^5	0.37	2.85	$7.8\times$
10%	10^6	1.71	9.80	$5.7\times$
100%	10^5	4.86	15.40	$3.2\times$
100%	10^6	7.13	24.26	$3.4\times$

that are common prefixes found in many clinical notes. For example, in a corpus containing repeated templates such as “Patient name: Alice Smith. Diagnosis: ...”, fine-tuning can increase the likelihood of “Alice Smith” after the prefix “Patient name:” relative to a held-out name; if the same template instead contains “Bob Jones,” the amplified identifier changes accordingly, but the mechanism is unchanged. Similarly, replacing most names with placeholders reduces the learned name prior, whereas leaving a small residual fraction creates a tail of identifiers whose probabilities may still be amplified. There may be some variation in leakage magnitude, due to differences in the total number of residual direct identifiers, their frequency, and the alignment between the clinical notes and attack prompts. Nevertheless, any clinical note containing residual direct identifiers when used in supervised fine-tuning presents a potential memorization risk that can be measured using our framework.

A central question for releasing API access to models fine-tuned on clinical notes is how to assess privacy risk when de-identification is known to be imperfect. In practice, institutions must decide whether a model can be safely queried without knowing which, if any, patient identifiers remain in the training data. Our framework speaks directly to this challenge by enabling an empirical assessment of whether a model exposes recoverable identifiers through interaction. Concretely, it provides a way to measure potential leakage and to use those signals to inform access decisions and mitigation efforts. It can also evaluate operational safeguards, such as rate limits, monitoring, and output filters, by comparing how they affect verified extraction success before and after implementing such safeguards. While this does not guarantee the absence of all residual identifiers, it offers a practical basis for evaluating and managing privacy risk when granting API access to clinical language models.

Privacy risk assessment before deployment is critical because undetected identifier leakage in real-world use may have regulatory repercussions. In the US, verified extraction of patient identifiers can trigger regulatory incident-response obligations; under the HIPAA Breach Notification Rule, covered entities must notify affected individuals without unreasonable delay and no later than 60 days after discovery of a breach, and breaches affecting 500+ individuals also require notification to HHS and prominent media outlets ([U.S. Department of Health & Human Services, 2013](#); [U.S. Government Publishing Office, a,b](#)).

Beyond the technical evaluation of privacy risk, governance decisions depend on the applicable regulatory framework, which differs both in terminology and legal framing across regions: for example, HIPAA specifies methods for *de-identifying* protected health information in the USA, whereas the GDPR (European Parliament and Council of the European Union, 2016) frames *anonymization* through an identifiability standard in EU. Our framework is therefore intended to provide reproducible evidence that can be interpreted by institutional governance bodies according to the applicable jurisdiction, their own policies, and their risk tolerance.

5.1. Limitations and future work

Our work is a baseline method to quantify direct identifier leakage in a controlled setting. The results should be read as characterizing leakage under our specific threat model rather than as definitive privacy guarantees.

Identifier scope. We focus on direct identifiers in the form of patient names. The risk to patient privacy also involves leakage of other direct identifiers (e.g., phone numbers, addresses) and quasi-identifiers that enable linkage with auxiliary data.

Prompting strategy and extracted stream shift. Our evaluation uses a fixed prompt family and simple sampling, including an explicitly extractive prompt (e.g., "Name:") intended to probe a worst-case querying scenario. In regimes with strong overfitting or very few direct identifiers, the model may produce non-canonical name-like outputs (e.g., variants, partial names, or formatting artifacts) that lie outside the candidate set, creating additional false-positive channels.

Model diversity and assumptions. We evaluate only two model sizes, 1 billion parameters and 8 billion parameters. The results may not extrapolate to larger models or other model families. Leakage patterns may vary under alternative adaptation strategies (e.g., parameter-efficient tuning methods such as LoRA (Hu et al., 2022)), different backbone models, stronger regularization, or privacy-preserving training methods. Besides, while our verifier relies on labeled member and non-member identifier subsets in our controlled experiments, an important direction for future work is to reduce labeling requirements and to study settings with more limited model access.

Adversarial fine-tuning against adaptive prompt attacks. A key next step is to explicitly model an adaptive adversary that optimizes prompts, decoding parameters, and multi-turn interaction policies to maximize identifier yield under a fixed query budget. Complementary to stronger attacks, an important direction is to fine-tune or train models to resist identifier extraction while preserving utility. One approach is adversarial training in which a prompt-optimizing attacker is trained (or approximated) alongside the model, and the model is optimized to reduce identifier emission under a broad distribution of queries.

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